
MASRCH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 21 18:50:59 1997; MasPar time 11.31 Seconds
 639.201 Million cell updates/sec

Tabular output not generated.

Title: >US-08-469-637-2
 Description: (1-390) from US08469637.pep (1 of 2)
 Perfect Score: 2927
 Sequence: 1 MNKLLCCALVFLDISIKWTT.....VPSQLHNVQIVSEVIFRNDR 390

Scoring table: PAM 150
 Gap 11

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot33
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10

Statistics: Mean 47.266; Variance 77.924; scale 0.607

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query				ID	Description	Pred. No.
	No.	Score	Match	Length DB			
1	405	13.8	461	9	TNR2_HUMAN	TUMOR NECROSIS FACTOR	1.65e-65
2	375	12.8	474	9	TNR2_MOUSE	TUMOR NECROSIS FACTOR	1.58e-58
3	303	10.4	277	2	CD40_HUMAN	CD40L RECEPTOR PRECUR	4.15e-42
4	294	10.0	305	2	CD40_MOUSE	CD40L RECEPTOR PRECUR	4.26e-40

5	269	9.2	326	9	VT2_MYXVL	TUMOR NECROSIS FACTOR	1.43e-34
6	260	8.9	325	9	VT2_SFVKA	TUMOR NECROSIS FACTOR	1.32e-32
7	260	8.9	435	9	TNRL_HUMAN	LYMPHOTOXIN-BETA RECE	1.32e-32
8	233	8.0	349	9	VC22_VARV	PROTEIN C22/B28 HOMOL	8.41e-27
9	221	7.6	454	9	TNR1_MOUSE	TUMOR NECROSIS FACTOR	2.86e-24
10	220	7.5	461	9	TNR1_RAT	TUMOR NECROSIS FACTOR	4.63e-24
11	215	7.3	416	6	NGFR_CHICK	LOW-AFFINITY NERVE GR	5.12e-23
12	213	7.3	427	6	NGFR_HUMAN	LOW-AFFINITY NERVE GR	1.33e-22
13	207	7.1	425	6	NGFR_RAT	LOW-AFFINITY NERVE GR	2.32e-21
14	178	6.1	595	2	CD30_HUMAN	CD30L RECEPTOR PRECUR	1.62e-15
15	172	5.9	455	9	TNR1_HUMAN	TUMOR NECROSIS FACTOR	2.42e-14
16	159	5.4	256	1	41BB_MOUSE	4-1BB LIGAND RECEPTOR	7.53e-12
17	159	5.4	260	2	CD27_HUMAN	CD27L RECEPTOR PRECUR	7.53e-12
18	146	5.0	271	6	OX40_RAT	OX40L RECEPTOR PRECUR	1.96e-09
19	144	4.9	272	6	OX40_MOUSE	OX40L RECEPTOR PRECUR	4.52e-09
20	140	4.8	255	1	41BB_HUMAN	4-1BB LIGAND RECEPTOR	2.38e-08
21	141	4.8	277	6	OX40_HUMAN	OX40L RECEPTOR PRECUR	1.57e-08
22	137	4.7	327	3	FASA_MOUSE	FASL RECEPTOR PRECURS	8.14e-08
23	134	4.6	250	2	CD27_MOUSE	CD27L RECEPTOR PRECUR	2.75e-07
24	134	4.6	335	3	FASA_HUMAN	FASL RECEPTOR PRECURS	2.75e-07
25	124	4.2	103	9	VA53_VACCV	PROTEIN A53.	1.44e-05
26	124	4.2	103	9	VA53_VACCC	PROTEIN A53.	1.44e-05
27	115	3.9	360	10	YIH9_YEAST	HYPOTHETICAL 41.6 KD	4.40e-04
28	105	3.6	2813	9	VWF_HUMAN	VON WILLEBRAND FACTOR	1.62e-02
29	102	3.5	3084	5	LMA1_MOUSE	LAMININ ALPHA-1 CHAIN	4.59e-02
30	100	3.4	1752	3	DESP_HUMAN	DESMOPLAKIN I AND II	9.05e-02
31	96	3.3	1104	8	SYV_YEAST	VALYL-TRNA SYNTHETASE	3.42e-01
32	96	3.3	1356	5	KAB7_YEAST	PROBABLE SERINE/THREO	3.42e-01
33	98	3.3	1947	6	MYSC_CAEEL	MYOSIN HEAVY CHAIN C	1.77e-01
34	96	3.3	2767	9	THYG_HUMAN	THYROGLOBULIN PRECURS	3.42e-01
35	96	3.3	3707	6	PGBM_MOUSE	BASEMENT MEMBRANE-SPE	3.42e-01
36	97	3.3	4092	3	DYHC_YEAST	DYNEIN HEAVY CHAIN, C	2.46e-01
37	94	3.2	122	9	VC22_VACCC	PROTEIN C22/B28.	6.54e-01
38	95	3.2	125	9	TNPF_STA AU	TRANSPOSASE FOR TRANS	4.73e-01
39	93	3.2	218	5	MERB_BACSR	ALKYLMERCURY LYASE (E	9.00e-01
40	95	3.2	916	8	RTJK_DROME	RNA-DIRECTED DNA POLY	4.73e-01
41	93	3.2	1122	9	TIE2_MOUSE	TYROSINE-PROTEIN KINA	9.00e-01
42	93	3.2	1429	5	LI12_CAEEL	LIN-12 PROTEIN PRECUR	9.00e-01
43	94	3.2	1609	5	LMG1_HUMAN	LAMININ GAMMA-1 CHAIN	6.54e-01
44	94	3.2	1966	6	MYSB_CAEEL	MYOSIN HEAVY CHAIN B	6.54e-01
45	95	3.2	2769	9	THYG_BOVIN	THYROGLOBULIN PRECURS	4.73e-01

ALIGNMENTS

RESULT 1

ID TNR2_HUMAN STANDARD; PRT; 461 AA.

AC P20333;

DT 01-FEB-1991 (REL. 17, CREATED)

DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR

DE BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B).

GN TNFR2 OR TNFR.

OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90260639.
 RA SMITH C.A., DAVIS T., ANDERSON D., SOLAM L., BECKMANN M.P., JERZY R.,
 RA DOWER S.K., COSMAN D., GOODWIN R.G.;
 RL SCIENCE 248:1019-1023(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91045991.
 RA KOHNO T., BREWER M.T., BAKER S.L., SCHWARTZ P.E., KING M.W.,
 RA HALE K.K., SQUIRES C.H., THOMPSON R.C., VANNICE J.L.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:8331-8335(1990).
 RN [3]
 RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE; 90349572.
 RA HELLER R.A., SONG K., ONASCH M.A., FISCHER W.H., CHANG D.,
 RA RINGOLD G.M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:6151-6155(1990).
 RN [4]
 RP SEQUENCE OF 27-31.
 RX MEDLINE; 90110215.
 RA ENGELMANN H., NOVICK D., WALLACH D.;
 RL J. BIOL. CHEM. 265:1531-1536(1990).
 RN [5]
 RP SEQUENCE OF 22-40; 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE; 91056048.
 RA LOETSCHER H., SCHLAEGER E.J., LAHM H.-W., PAN Y.-C.E., LESSLAUER W.,
 RA BROCKHAUS M.;
 RL J. BIOL. CHEM. 265:20131-20138(1990).
 RN [6]
 RP CHARACTERIZATION.
 RX MEDLINE; 93016040.
 RA PENNICA D., LAM V.T., MIZE N.K., WEBER R.F., LEWIS M., FENDLY B.M.,
 RA LIPARI M.T., GOEDEL D.V.;
 RL J. BIOL. CHEM. 267:21172-21178(1992).
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 CC -!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 CC LEVEL ON THREONINE RESIDUES.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; M32315; G189186; -.
 DR EMBL; M35857; G339752; -.
 DR EMBL; M55994; G339758; -.
 DR PIR; A35356; A35356.
 DR PIR; A36007; A36007.
 DR PIR; A36475; A36475.
 DR PIR; B35010; B35010.
 DR PIR; A23666; A23666.
 DR HSSP; P19438; 1TNR.
 DR MIM; 191191; 11TH EDITION.

DR PROSITE; PS00652; TNFR_NGFR.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL;
KW PHOSPHORYLATION.
FT SIGNAL 1 22
FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 258 287 POTENTIAL.
FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 201 4 X TNFR-CYS.
FT REPEAT 39 76 TNFR-CYS 1.
FT REPEAT 77 118 TNFR-CYS 2.
FT REPEAT 119 162 TNFR-CYS 3.
FT REPEAT 163 201 TNFR-CYS 4.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 57 75 BY SIMILARITY.
FT DISULFID 78 93 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 POTENTIAL.
FT CARBOHYD 193 193 POTENTIAL.
FT CONFLICT 141 141 R -> P (IN REF. 3).
FT CONFLICT 196 196 R -> M (IN REF. 1).
FT CONFLICT 363 363 A -> T (IN REF. 3).
SQ SEQUENCE 461 AA; 48316 MW; 0F5D0C44 CRC32;

Query Match 13.8%; Score 405; DB 9; Length 461;
Best Local Similarity 41.8%; Pred. No. 1.65e-65;
Matches 69; Conservative 26; Mismatches 59; Indels 11; Gaps 8;

Db 45 yydqta-qmccskcspgghakvfctktsdtvcdscdstyqlwnwvpeclscgsrccsd 103
| ::| :| :| ||:| | || ||| :| | ||: | : ||| |:: |
Qy 31 YDEETSHQLLCDKCPPGYLKHQHTAKWKTVCAPCPDHYTDSWHTSDECLYCSPVCKEL 90
Db 104 qvetqactreqnrictcrpgwycalskqegcrlcaplrkcrpgfgvârpqgtâtsdvâckp 163
| | | :||:| | :| | | | | | | | | | :|| : |||
Qy 91 QYVKQECNRTHNRVCECKEGRY--LEI-EFC-L-KH-RSCPPGFGVQAGTPERNTVCKR 144
Db 164 capgtfsnttsstdicrphqicnvvai---p-gnasrdavctsts 204
| : | ||| | | | | | :| : : ||| :| :| :| :|
Qy 145 CPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS 189

RESULT 2
ID TNR2_MOUSE STANDARD; PRT; 474 AA.
AC P25119;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).

GN TNFR-2.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91187885.
 RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
 RA WONG G.H., CHEN E.Y., GOEDDEL D.V.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91246168.
 RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
 RA COPELAND N.G., JENKINS N.A., SMITH C.A.;
 RL MOL. CELL. BIOL. 11:3020-3026 (1991).
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; M60469; G199828; -.
 DR EMBL; M59378; G202095; -.
 DR PIR; B38634; B38634.
 DR HSSP; P19438; 1TNR.
 DR PROSITE; PS00652; TNFR_NGFR.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 22
 FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
 FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 259 288 POTENTIAL.
 FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 39 203 4 X TNFR-CYS.
 FT REPEAT 39 77 TNFR-CYS 1.
 FT REPEAT 78 119 TNFR-CYS 2.
 FT REPEAT 120 164 TNFR-CYS 3.
 FT REPEAT 165 203 TNFR-CYS 4.
 FT DISULFID 40 54 BY SIMILARITY.
 FT DISULFID 55 68 BY SIMILARITY.
 FT DISULFID 58 76 BY SIMILARITY.
 FT DISULFID 79 94 BY SIMILARITY.
 FT DISULFID 97 111 BY SIMILARITY.
 FT DISULFID 101 119 BY SIMILARITY.
 FT DISULFID 121 127 BY SIMILARITY.
 FT DISULFID 136 145 BY SIMILARITY.
 FT DISULFID 139 163 BY SIMILARITY.
 FT DISULFID 166 181 BY SIMILARITY.
 FT CARBOHYD 69 69 POTENTIAL.
 FT CARBOHYD 195 195 POTENTIAL.
 SQ SEQUENCE 474 AA; 50319 MW; DC32B2B6 CRC32;

Query Match 12.8%; Score 375; DB 9; Length 474;
 Best Local Similarity 41.5%; Pred. No. 1.58e-58;
 Matches 66; Conservative 21; Mismatches 61; Indels 11; Gaps 7;

Db 52 qmccakcpgpggyvkhfcnksdtvcadceasmtyqvwngfrtclscsssccttdqveirac 111

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      | : | | | | | | : | : | | | | | | : | : | | | : | | : |
Qy    38 QLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECLYCSPVCKELQYVKQEC 97

Db    112 tkqqrncvaceagrycalkthsgscrqcmrlskcpgpgfgvassrapngnvlckacapgtf 171
      : : | | | | | | | | | | | | | | | | : : | : | : | : |
Qy    98 NRTHNRVCECKEGRY--LEIEF--CLKH-R-S-CPPGFGVVQAGTPERN TVCKRCPDGFF 150

Db    172 sdttsstdvcrphricsi--laip--gnastdavcapes 206
      | : | | | | | | | | : | : | | | : | : | : |
Qy    151 SNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS 189

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RESULT 3

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ID    CD40_HUMAN          STANDARD;          PRT;    277 AA.
AC    P25942;
DT    01-MAY-1992 (REL. 22, CREATED)
DT    01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT    01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE    CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
GN    CD40.
OS    HOMO SAPIENS (HUMAN).
OC    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC    EUTHERIA; PRIMATES.
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE; 89356608.
RA    STAMENKOVIC I., CLARK E.A., SEED B.;
RL    EMBO J. 8:1403-1410(1989).
CC    -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC    -!- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC    -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR    EMBL; X60592; G29851; -.
DR    PIR; S04460; S04460.
DR    MIM; 109535; 11TH EDITION.
DR    PROSITE; PS00652; TNFR_NGFR.
KW    RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
FT    SIGNAL              1      19      POTENTIAL.
FT    CHAIN               20     277     CD40L RECEPTOR.
FT    DOMAIN              20     193     EXTRACELLULAR (POTENTIAL).
FT    TRANSMEM            194     215     POTENTIAL.
FT    DOMAIN              216     277     CYTOPLASMIC (POTENTIAL).
FT    DOMAIN              25     187     4 X TNFR-CYS.
FT    REPEAT              25      60     TNFR-CYS 1.
FT    REPEAT              61     103     TNFR-CYS 2.
FT    REPEAT             104     144     TNFR-CYS 3.
FT    REPEAT             145     187     TNFR-CYS 4.
FT    CARBOHYD            153     153     POTENTIAL.
FT    CARBOHYD            180     180     POTENTIAL.
SQ    SEQUENCE    277 AA;  30619 MW;  3B284411 CRC32;

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Query Match          10.4%;  Score 303;  DB 2;  Length 277;
Best Local Similarity 36.8%;  Pred. No. 4.15e-42;
Matches      56;  Conservative 21;  Mismatches 67;  Indels 8;  Gaps 7;

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Db 38 cs1cqpqgqklvsdcteftetec1pcgesefldtnwrethchqhkycdpn-lglr-vqqkg 95
 | | | | | | | | : : : : | | | : | |
 Qy 41 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDEC-L--YCSPVCKELQYVKQEC 97

 Db 96 tsetdtictceegwhctseacescvlhrscspgfgvkqiatgvsdticepcpvgffsnvs 155
 : : | | | : | | : | | : | | | | : | : | | | | :
 Qy 98 NRTHNRVCECKEGRY-L-EI-EFCLKHRSCPPGFGVVQAGTPERN TVCKRCPDGGFFSNET 154

 Db 156 safekchpwtscetkdlvvqqagtnktdvvcg 187
 | : | : | : | : | : | : | : | : | :
 Qy 155 SSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 186

RESULT 4

ID CD40_MOUSE STANDARD; PRT; 305 AA.
 AC P27512;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
 GN CD40.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92105763.
 RA TORRES R.M., CLARK E.A.;
 RL J. IMMUNOL. 148:620-626(1992).
 CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; M83312; G192520; -.
 DR PIR; A46476; A46476.
 DR HSSP; P19438; 1TNR.
 DR PROSITE; PS00652; TNFR_NGFR.
 KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 305 CD40L RECEPTOR.
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 194 215 POTENTIAL.
 FT DOMAIN 216 305 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 187 4 X TNFR-CYS.
 FT REPEAT 25 60 TNFR-CYS 1.
 FT REPEAT 61 103 TNFR-CYS 2.
 FT REPEAT 104 144 TNFR-CYS 3.
 FT REPEAT 145 187 TNFR-CYS 4.
 FT CARBOHYD 153 153 POTENTIAL.
 SQ SEQUENCE 305 AA; 33617 MW; 781C241D CRC32;

Query Match 10.0%; Score 294; DB 2; Length 305;
 Best Local Similarity 38.8%; Pred. No. 4.26e-40;
 Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;

Db 38 cdlcqpgsrltshctalektqchpcdsgefsaqwnreirchqhrhcepn-qggr-vkkeg 95
 || | ||: | ||| || | || :: |: | | | : || |
 Qy 41 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKELQYVKQEC 97

 Db 96 taesdtvctckegqhctskdceacaqhtpcipgfgvmematettdtvchpcpvvgffsnqs 155
 : || |||: : | | | : | ||||:: : | : || | || ||||:::
 Qy 98 NRTHNRVCECKEGRY-L--EIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNET 154

 Db 156 slfekcypwtscedknlevlqkgtsqtnvicg 187
 | | | : | : ||| : : ||:
 Qy 155 SSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 186